

MRLEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR
PCRRDSP TTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF
AHAGFCLEHASCPPGAGVIAPGTPS QNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA
LNVPGSSSHDTLCTSGTFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLQLALEAPE
GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLQLALRVARMPGLERSVRERFLPVH

Fig. 1

"I have been thinking about you very much lately,"

Fig. 3

SEQ ID No: 4 128 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 SEQ ID No: 5 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 SEQ ID No: 6 1
 SEQ ID No: 3 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 G
 SEQ ID No: 4 178 CA-TTCTGGAACCTACCTGGAGCGC
 SEQ ID No: 5 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCCTCTGNNG
 SEQ ID No: 6 2 CAGTTCTGGAACCTACCTGGAGCNCCTGCCGCTACTGCAACGTCCTCTGCGG
 SEQ ID No: 3 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCCTCTGNNG
 SEQ ID No: 5 101 GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAAACCGGCCT
 SEQ ID No: 6 52 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAAACCGTGCCCT
 SEQ ID No: 7 1 GAGGGCCCCCAGGAGTGCGTGGCGGAGGTG
 SEQ ID No: 3 101 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAAACCGTGCCCT
 SEQ ID No: 5 151 GCNGCTGCAGCACCGGNTTCTTCGCGCACGCTGNTTCTGCTTGGAGCAC
 SEQ ID No: 6 102 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTCTGCTTGGAGCAC
 SEQ ID No: 7 32 TGGCAGGGGTACAGTTGCTGGTCCCGCCTTGACCCCTGACCTAGCTAGGACAC
 SEQ ID No: 3 151 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTCTGCTTGGAGCAC
 SEQ ID No: 5 201 GCATCGTGTCCACCTGGTGNCGGCGTGATTGNCNCCGGGCACCCCCAGCCA
 SEQ ID No: 6 152 GCATCGTGTCCACCTGGTGCAGGCGTGATTNCCCGGACACCCCCAGCCA
 SEQ ID No: 7 82 CAGTTCCCTGACCCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA
 SEQ ID No: 8 1 GCATCGTGTCCACCTGGTGCAGGCGTGATTGCCCCGGGCACCCCCAGCCA
 SEQ ID No: 10 1 CTTGTCCACCTGGTGCAGGCGTGATTNCCC-GGGACCCCCAGCCA
 SEQ ID No: 3 201 GCATCGTGTCCACCTGGTGCAGGCGTGATTGCCCCGGGCACCCCCAGCCA

Fig. 4

SEQ ID NO: 5 251 GAACACGCA - TGCAAAAGCCGTG
 SEQ ID NO: 7 132 GAACACGAGN - CC - AGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 8 51 GAACACGAG - GCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 10 47 GAACACGAGTGCC - AGCCNT - CCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 9 1 AGCNGTGCCNCCNAGGCACCTTCTCAGCCAGCAGT
 SEQ ID NO: 3 251 GAACACGAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 7 182 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 8 101 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 10 97 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 9 36 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 3 301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 7 232 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAG
 SEQ ID NO: 8 151 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAG
 SEQ ID NO: 10 147 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 9 86 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 3 351 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 10 197 GCACTGGCTTCCCCCTCAGCACCCAGGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 9 136 GCACTGGCTTCCCCCTCAGCACCCAGGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 3 401 GCACTGGCTTCCCCCTCAGCACCCAGGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 10 247 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT
 SEQ ID NO: 9 186 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT
 SEQ ID NO: 3 451 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT

Fig. 4 (cont.)

UNA 30942
HINFR2

MRALCEPGLISLLGLVIALPALLPVPAVRGVATIPITYPWRD·AEIG
MAPVAVWALAVGLELWAAAHALPADVAFFPYAPLPGSTCRLREYYDOI

DNA 30942
HINFR2

CRD1
45 ERLVCAQCPCPGTFVORPCRRDSPITCGPCPPRH YTOFWNYLERCRYCNVL
50 AOMCCSKCSPGQNAKVFCTKTS DTVCDSCGEOSTYTQIWNWVPECLSCGSR

DNA 30942
HINFR2

CRD2
75 CGEREEEARACHATHNRACRCRTGFF...AHAG...FCLHASCPPGAGV
100 CSSDOVETOACTREQNRICTCRPGWYCALSKOEGCRLCAPLRKCRPGFGV

DNA 30942
HINFR2

CRD3
139 IAPGTPSONTCQPCPPGTFSSASSSSEQCOPHRNCTALGLALNVPGSSS
150 ARPGETETSDVCKPCA PGTFSSNTTSSSTDCRPHQICNVVA...IPGNAS

DNA 30942
HINFR2

CRD4
189 HDTLCTSTCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLORLLOALEA
196 RDAVCTSTS...PTRSMAPGAVHLPQPVSTRSQHTOPTPEPSTAPSTSFL

DNA 30942
HINFR2

229 PEGWGPTP...RAGRAALOLKLRRLTELLGAODGALLVRLLOALRVAMP
241 PMGPSPPAEGSTGDFALPVGLIVGVTA LGLLIIGVVNCVIMTQVKKKPL

DNA 30942
HINFR2

287 GLERSVRERFLPVH
293 CLQREAKVPHLPADKARGTQGPEOQHLITAPSSSSSSLESSASALD-RRA

HINFR2

343 PTRNOPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD

HINFR2

393 HSSQCSSQASSTMGDTDSSPSES PKDEQVPFSKEECAFRSOLETPETLLG

HINFR2

443 STEEKPLPLGVPOAGMKPS

Fig. 5

DcR3 1 M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A 31
 OPG 1 M N K L L C C A L V F L D I S I K W T T Q E T F P - - - - - 25

CRD1

DcR3 32 E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C 62
 OPG 26 - - P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C 54

DcR3 63 R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V 93
 OPG 55 T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P 85

CRD2

DcR3 94 L C G E R E E E A R A C H A T H N R A C R C R T G F F A H A G 124
 OPG 86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E 116

CRD3

DcR3 125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P 155
 OPG 117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D 147

CRD4

DcR3 156 G T F S A S S S S S E Q C Q P H R N C T A L G L A L N V P G S 186
 OPG 148 G F F S N E T S S K A P C R K H T N C S V F G L L L T Q K G N 178

DcR3 187 S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D 217
 OPG 179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R 208

DcR3 218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R 247
 OPG 209 F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R 239

DcR3 248 A G R A A L Q L K L R R R L T E L L G A Q D G A L - L V R L L 277
 OPG 240 I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I 270

DcR3 278 Q A L R V A R M P G L E R S V R E R F L P V H 300
 OPG 271 I Q D I D L C E N S V Q R H I G H A N L T F E 293...

Fig. 6

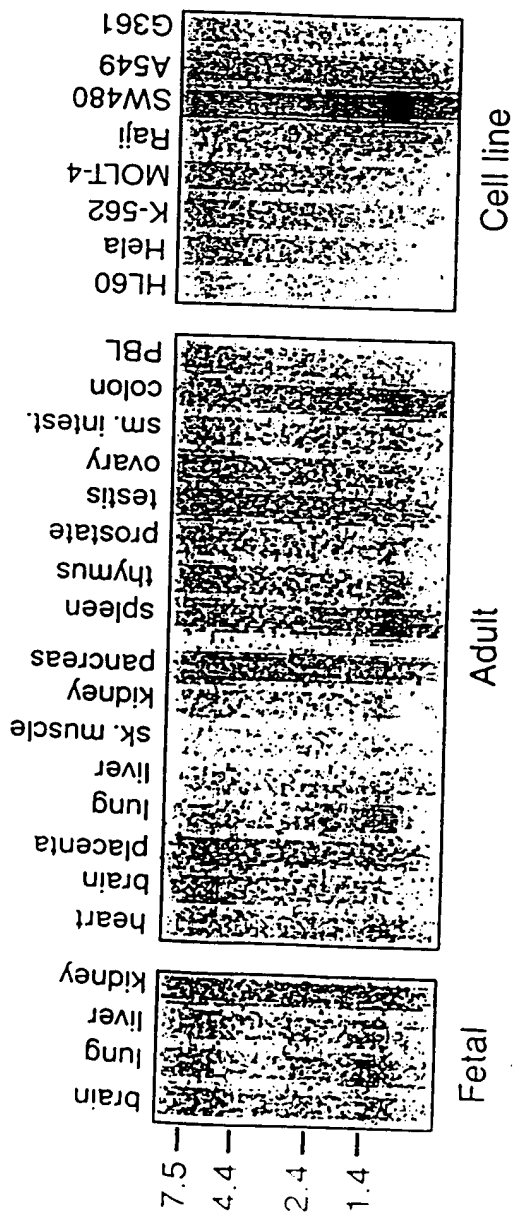


Fig. 7

338T60"002LST60

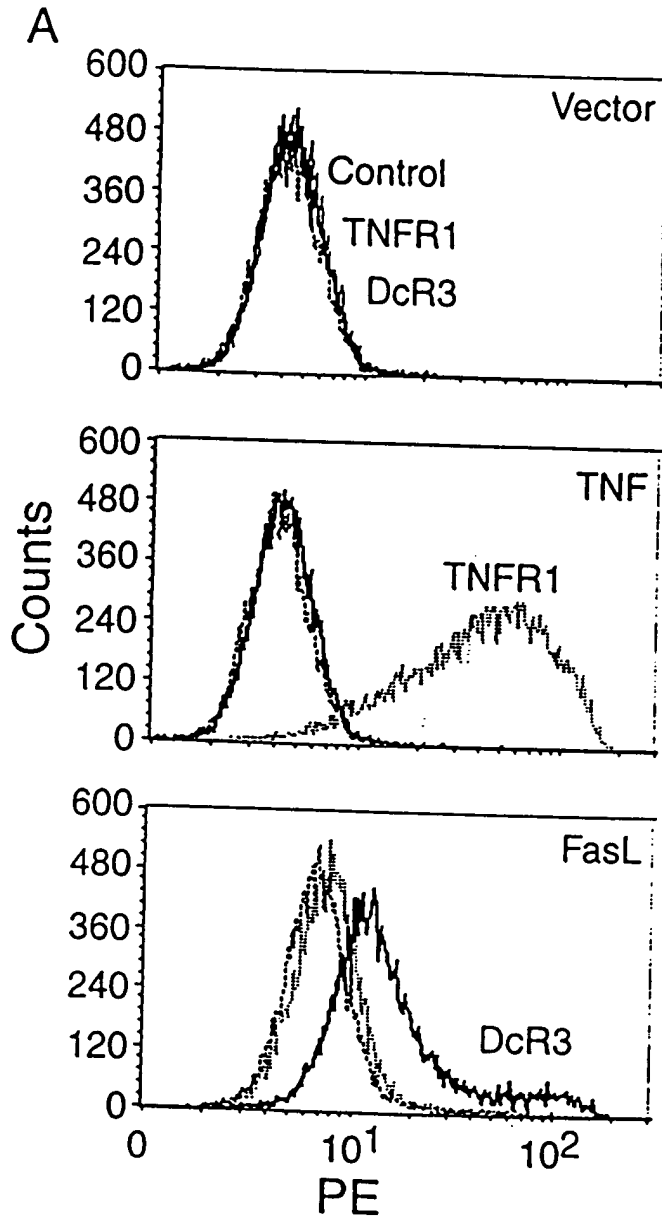
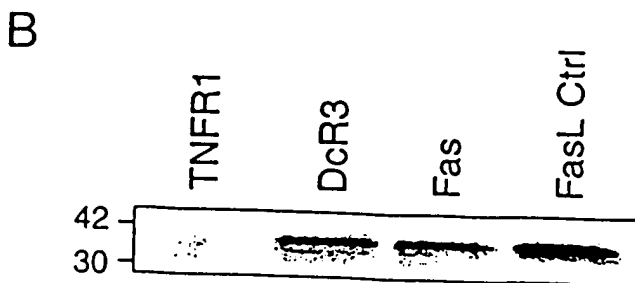


Fig. 8



63760-63760

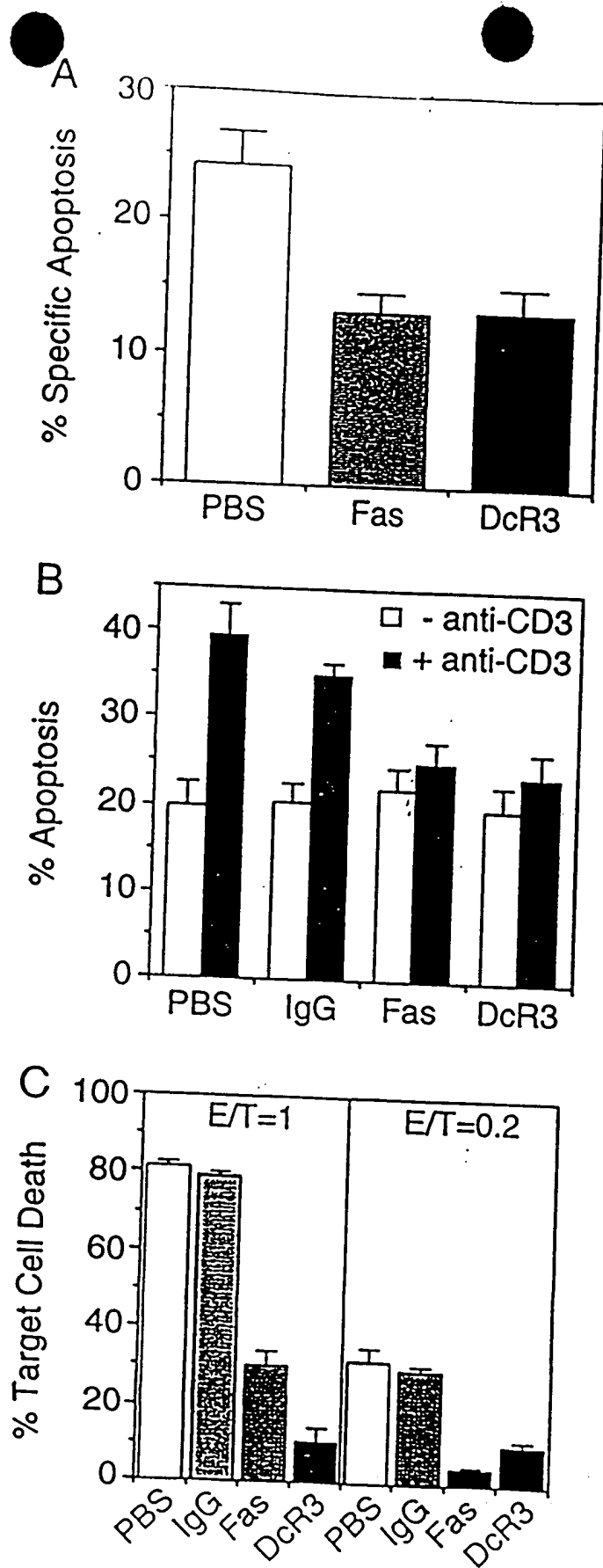


Fig. 9

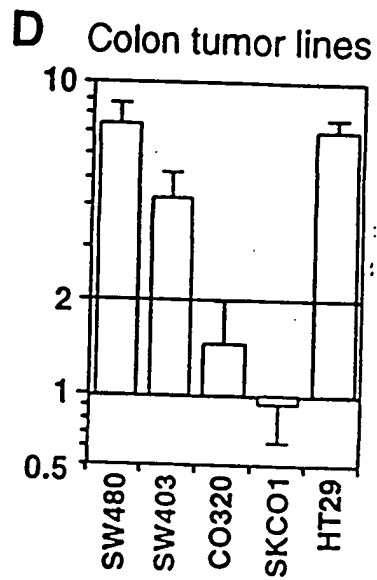
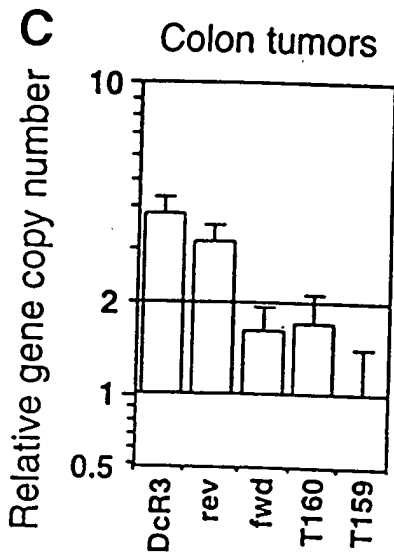
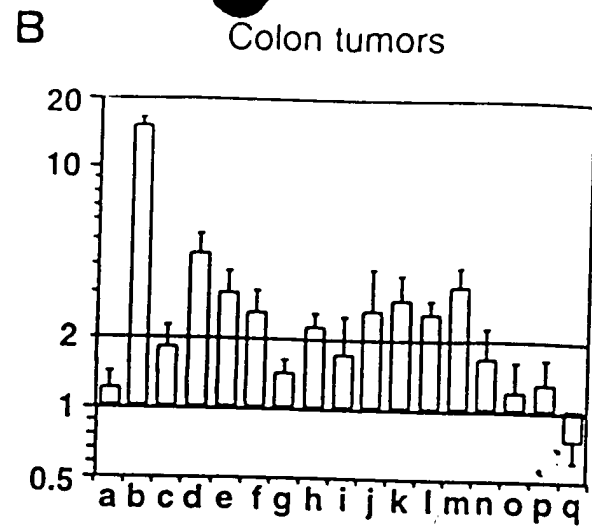
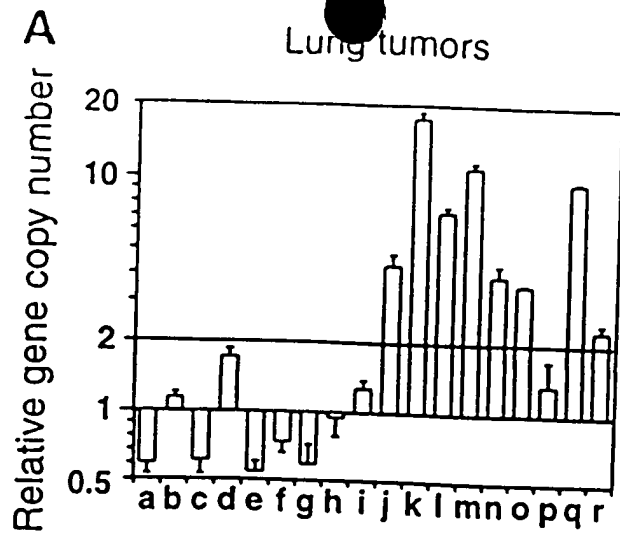


Fig. 10

09457280-094595

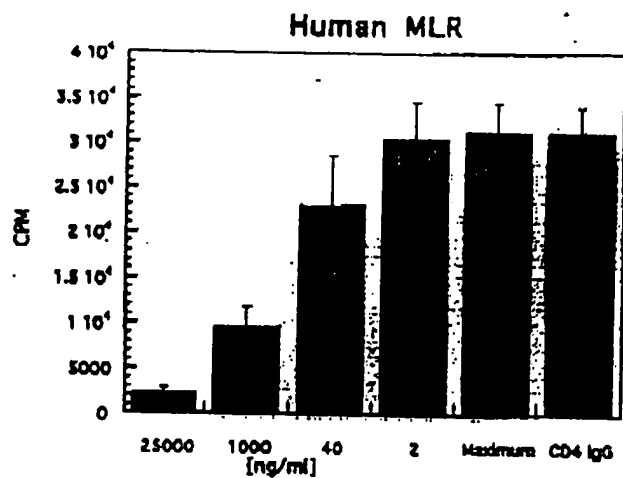


Fig. 11A

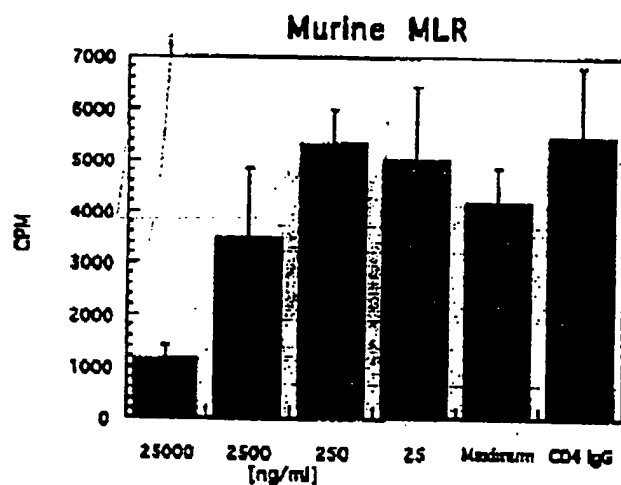


Fig. 11B

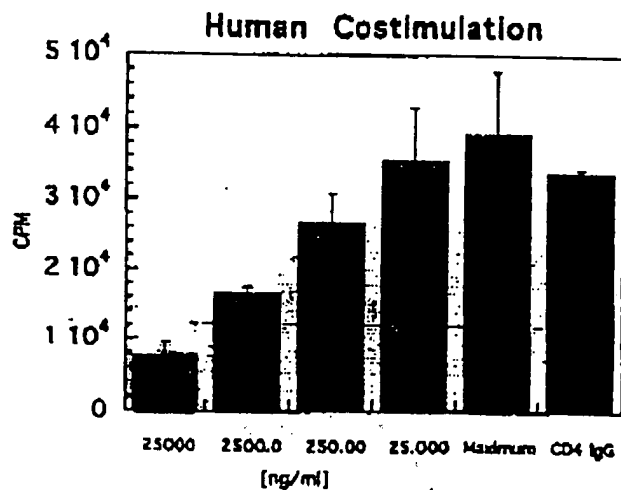







Fig. 11C

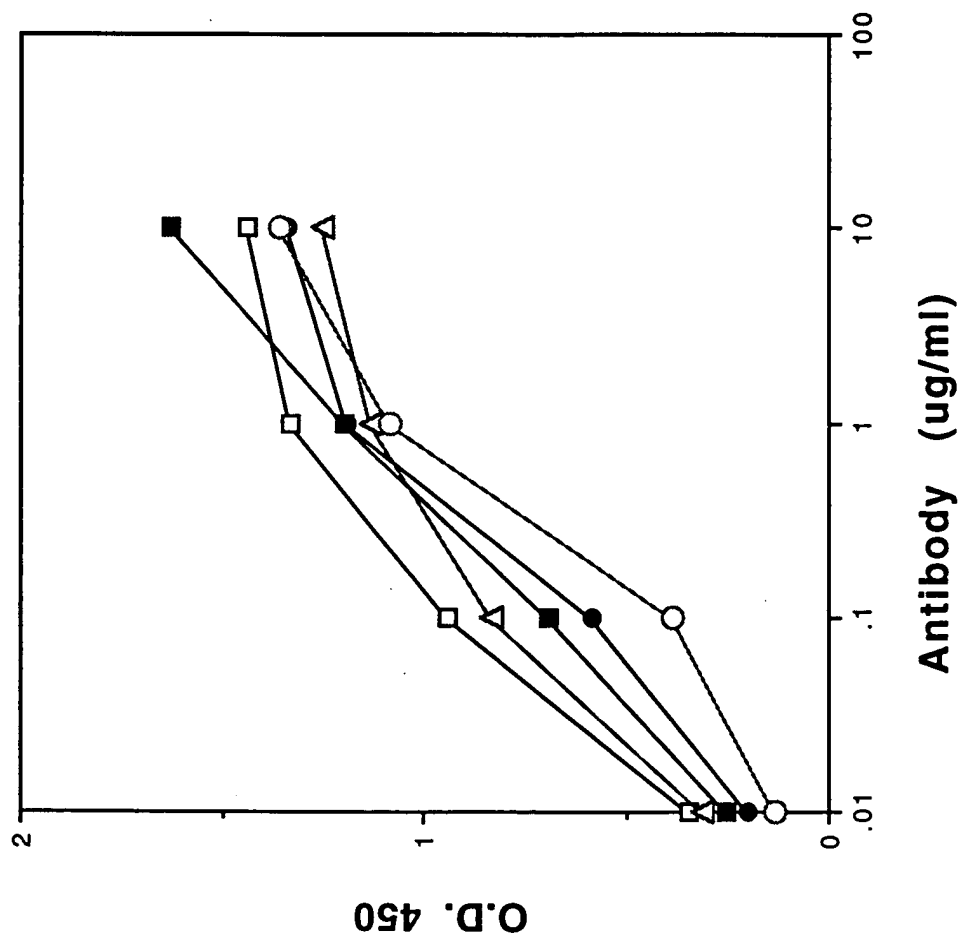
FIGURE 12

<u>mAb</u>	<u>Isotype</u>	<u>Antigen Specificity (ELISA)</u>					% Blocking (ELISA)
		<u>DcR3</u>	<u>DR4</u>	<u>DR5</u>	<u>DcR1</u>	<u>OPG</u>	
4B7.1.1	IgG1	+++	-	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.

% blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

 4B7, 1, 1
 4C4, 1, 4
 5C4, 14, 7
 8D3, 1, 5
 11C5, 2, 8



13

Fig. 14

